

Sequence Listing

<110> Adams, Sean
Pan, James
Zhong, Alan

<120> UCP4

<130> P1626R1

<141> 1999-09-15

<150> US 60/101,279

<151> 1998-09-22

<150> US 60/114,223

<151> 1998-12-30

<150> US 60/129,674

<151> 1999-04-16

<160> 18

<210> 1

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<212> PRT

<213> Homo sapiens

<400> 1

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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser

				110					115					120
Glu	Asp	Glu	His	Tyr 125	Pro	Leu	Trp	Lys	Ser 130	Val	Ile	Gly	Gly	Met 135
Met	Ala	Gly	Val	Ile 140	Gly	Gln	Phe	Leu	Ala 145	Asn	Pro	Thr	Asp	Leu 150
Val	Lys	Val	Gln	Met 155	Gln	Met	Glu	Gly	Lys 160	Arg	Lys	Leu	Glu	Gly 165
Lys	Pro	Leu	Arg	Phe 170	Arg	Gly	Val	His	His 175	Ala	Phe	Ala	Lys	Ile 180
Leu	Ala	Glu	Gly	Gly 185	Ile	Arg	Gly	Leu	Trp 190	Ala	Gly	Trp	Val	Pro 195
Asn	Ile	Gln	Arg	Ala 200	Ala	Leu	Val	Asn	Met 205	Gly	Asp	Leu	Thr	Thr 210
Tyr	Asp	Thr	Val	Lys 215	His	Tyr	Leu	Val	Leu 220	Asn	Thr	Pro	Leu	Glu 225
Asp	Asn	Ile	Met	Thr 230	His	Gly	Leu	Ser	Ser 235	Leu	Cys	Ser	Gly	Leu 240
Val	Ala	Ser	Ile	Leu 245	Gly	Thr	Pro	Ala	Asp 250	Val	Ile	Lys	Ser	Arg 255
Ile	Met	Asn	Gln	Pro 260	Arg	Asp	Lys	Gln	Gly 265	Arg	Gly	Leu	Leu	Tyr 270
Lys	Ser	Ser	Thr	Asp 275	Cys	Leu	Ile	Gln	Ala 280	Val	Gln	Gly	Glu	Gly 285
Phe	Met	Ser	Leu	Tyr 290	Lys	Gly	Phe	Leu	Pro 295	Ser	Trp	Leu	Arg	Met 300
Thr	Pro	Trp	Ser	Met 305	Val	Phe	Trp	Leu	Thr 310	Tyr	Glu	Lys	Ile	Arg 315
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<210> 2
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<212> DNA
<213> Homo sapiens
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tcttgctcgg ttgggagacg gtgcaagaga atctgcccc tataggggaa 250
tgggtgcgcac agccctaggg atcattgaag aggaaggctt tctaaagctt 300
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tcgaatggtc acatatgaac atctccgaga gggtgtgttt ggcaaaagtg 400
aagatgagca ttatccccctt tggaaatcag tcattggagg gatgatggct 450
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gatgcaaata gaaggaaaaa ggaaactgga aggaaaacca ttgcgatttc 550
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cagaataatg aatcaaccac gagataaaca aggaagggga cttttgtata 850
aatcatcgac tgactgcttg attcaggctg ttcaagggtga aggattcatg 900
agtctatata aaggcttttt accatcttgg ctgagaatga ccccttggtc 950
aatggtgttc tggcttactt atgaaaaaat cagagagatg agtggagtca 1000
gtccatttta agaattctgc agatatccat cacactggc 1039

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<211> 31

<212> DNA

<213> Artificial

<220>

<223> Artificial Sequence 1-31

<400> 3

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<211> 34
<212> DNA
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<220>
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cacaaaaact cgactccaaa tgcaaggaga agcagctctt gctcggttgg 200
gagacggtgc aagagaatct gccccctata ggggaatggg gcgcacagcc 250
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accgccatt tacagacag tagttatttc tggaggtcga atggtcacat 350
atgaacatct ccgagagggt gtgtttggca aaagtgaaga tgagcattat 400
cccctttgg aatcagtc atggaggatg atggctggtg ttattggcca 450
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gaaaaaggaa actggaagga aaaccattgc gatttcgtgg tgtacatcat 550
gcatttgcaa aaatcttagc tgaaggagga atacgaaggc tttgggcagg 600
ctgggtaccc aatatacaaa gagcagcact ggtgaatatg ggagatttaa 650

ccacttatga tacagtgaac cactacttgg tattgaatac accacttgag 700
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ctattccaca gagactgatt tatagggggc agcactttat ttttttctgg 1150
aaacccaagt tctctttgac tcctcttttt gtccaaaagt gatctgggtc 1200
gatctcaca ggccatccaa tgagaccccg nacagcattt tctaaaga 1248

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<213> Artificial

<220>
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ggaggagg 58

<210> 7
<211> 35
<212> DNA
<213> Artificial

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<210> 8
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<212> DNA
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<210> 12
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<212> DNA
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<220>
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<210> 13
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<220>
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<211> 23
<212> DNA
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<220>
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<210> 15
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<220>
<223> Artificial Sequence 1-22

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<210> 16
<211> 307
<212> PRT
<213> Homo sapiens

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20 25 30
Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly
35 40 45

Glu	Cys	Pro	Thr	Ser	Ser	Val	Ile	Arg	Tyr	Lys	Gly	Val	Leu	Gly		50	55	60
Thr	Ile	Thr	Ala	Val	Val	Lys	Thr	Glu	Gly	Arg	Met	Lys	Leu	Tyr		65	70	75
Ser	Gly	Leu	Pro	Ala	Gly	Leu	Gln	Arg	Gln	Ile	Ser	Ser	Ala	Ser		80	85	90
Leu	Arg	Ile	Gly	Leu	Tyr	Asp	Thr	Val	Gln	Glu	Phe	Leu	Thr	Ala		95	100	105
Gly	Lys	Glu	Thr	Ala	Pro	Ser	Leu	Gly	Ser	Lys	Ile	Leu	Ala	Gly		110	115	120
Leu	Thr	Thr	Gly	Gly	Val	Ala	Val	Phe	Ile	Gly	Gln	Pro	Thr	Glu		125	130	135
Val	Val	Lys	Val	Arg	Leu	Gln	Ala	Gln	Ser	His	Leu	His	Gly	Ile		140	145	150
Lys	Pro	Arg	Tyr	Thr	Gly	Thr	Tyr	Asn	Ala	Tyr	Arg	Ile	Ile	Ala		155	160	165
Thr	Thr	Glu	Gly	Leu	Thr	Gly	Leu	Trp	Lys	Gly	Thr	Thr	Pro	Asn		170	175	180
Leu	Met	Arg	Ser	Val	Ile	Ile	Asn	Cys	Thr	Glu	Leu	Val	Thr	Tyr		185	190	195
Asp	Leu	Met	Lys	Glu	Ala	Phe	Val	Lys	Asn	Asn	Ile	Leu	Ala	Asp		200	205	210
Asp	Val	Pro	Cys	His	Leu	Val	Ser	Ala	Leu	Ile	Ala	Gly	Phe	Cys		215	220	225
Ala	Thr	Ala	Met	Ser	Ser	Pro	Val	Asp	Val	Val	Lys	Thr	Arg	Phe		230	235	240
Ile	Asn	Ser	Pro	Pro	Gly	Gln	Tyr	Lys	Ser	Val	Pro	Asn	Cys	Ala		245	250	255
Met	Lys	Val	Phe	Thr	Asn	Glu	Gly	Pro	Thr	Ala	Phe	Phe	Lys	Gly		260	265	270
Leu	Val	Pro	Ser	Phe	Leu	Arg	Leu	Gly	Ser	Trp	Asn	Val	Ile	Met		275	280	285
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Gln Thr Met Asp Cys Ala Thr
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<210> 17
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				20					25					30
Thr	Phe	Pro	Leu	Asp	Thr	Ala	Lys	Val	Arg	Leu	Gln	Ile	Gln	Gly
				35					40					45
Glu	Ser	Gln	Gly	Pro	Val	Arg	Ala	Thr	Val	Ser	Ala	Gln	Tyr	Arg
				50					55					60
Gly	Val	Met	Gly	Thr	Ile	Leu	Thr	Met	Val	Arg	Thr	Glu	Gly	Pro
				65					70					75
Arg	Ser	Leu	Tyr	Asn	Gly	Leu	Val	Ala	Gly	Leu	Gln	Arg	Gln	Met
				80					85					90
Ser	Phe	Ala	Ser	Val	Arg	Ile	Gly	Leu	Tyr	Asp	Ser	Val	Lys	Gln
				95					100					105
Phe	Tyr	Thr	Lys	Gly	Ser	Glu	His	Ala	Ser	Ile	Gly	Ser	Arg	Leu
				110					115					120
Leu	Ala	Gly	Ser	Thr	Thr	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln
				125					130					135
Pro	Thr	Asp	Val	Val	Lys	Val	Arg	Phe	Gln	Ala	Gln	Ala	Arg	Ala
				140					145					150
Gly	Gly	Gly	Arg	Arg	Tyr	Gln	Ser	Thr	Val	Asn	Ala	Tyr	Lys	Thr
				155					160					165
Ile	Ala	Arg	Glu	Glu	Gly	Phe	Arg	Gly	Leu	Trp	Lys	Gly	Thr	Ser
				170					175					180
Pro	Asn	Val	Ala	Arg	Asn	Ala	Ile	Val	Asn	Cys	Ala	Glu	Leu	Val
				185					190					195
Thr	Tyr	Asp	Leu	Ile	Lys	Asp	Ala	Leu	Leu	Lys	Ala	Asn	Leu	Met
				200					205					210

Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala Gly
215 220 225

Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
230 235 240

Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His
245 250 255

Cys Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr
260 265 270

Lys Gly Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val
275 280 285

Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala
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Ala Cys Thr Ser Arg Glu Ala Pro Phe
305 309

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20 25 30

Ile Gln Gly Glu Asn Gln Ala Val Gln Thr Ala Arg Leu Val Gln
35 40 45

Tyr Arg Gly Val Leu Gly Thr Ile Leu Thr Met Val Arg Thr Glu
50 55 60

Gly Pro Cys Ser Pro Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg
65 70 75

Gln Met Ser Phe Ala Ser Ile Arg Ile Gly Leu Tyr Asp Ser Val
80 85 90

Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp Asn Ser Ser Leu Thr
95 100 105

Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala Met Ala Val Thr
110 115 120

065750-24E/6E60

Cys	Ala	Gln	Pro	Thr	Asp	Val	Val	Lys	Val	Arg	Phe	Gln	Ala	Ser	
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Ile	His	Leu	Gly	Pro	Ser	Arg	Ser	Asp	Arg	Lys	Tyr	Ser	Gly	Thr	
				140					145					150	
Met	Asp	Ala	Tyr	Arg	Thr	Ile	Ala	Arg	Glu	Glu	Gly	Val	Arg	Gly	
				155					160					165	
Leu	Trp	Lys	Gly	Thr	Leu	Pro	Asn	Ile	Met	Arg	Asn	Ala	Ile	Val	
				170					175					180	
Asn	Cys	Ala	Glu	Val	Val	Thr	Tyr	Asp	Ile	Leu	Lys	Glu	Lys	Leu	
				185					190					195	
Leu	Asp	Tyr	His	Leu	Leu	Thr	Asp	Asn	Phe	Pro	Cys	His	Phe	Val	
				200					205					210	
Ser	Ala	Phe	Gly	Ala	Gly	Phe	Cys	Ala	Thr	Val	Val	Ala	Ser	Pro	
				215					220					225	
Val	Asp	Val	Val	Lys	Thr	Arg	Tyr	Met	Asn	Ser	Pro	Pro	Gly	Gln	
				230					235					240	
Tyr	Phe	Ser	Pro	Leu	Asp	Cys	Met	Ile	Lys	Met	Val	Ala	Gln	Glu	
				245					250					255	
Gly	Pro	Thr	Ala	Phe	Tyr	Lys	Gly	Phe	Thr	Pro	Ser	Phe	Leu	Arg	
				260					265					270	
Leu	Gly	Ser	Trp	Asn	Val	Val	Met	Phe	Val	Thr	Tyr	Glu	Gln	Leu	
				275					280					285	
Lys	Arg	Ala	Leu	Met	Lys	Val	Gln	Met	Leu	Arg	Glu	Ser	Pro	Phe	
				290					295					300	